CLAIMS

1 (original)
A method for detecting a target nucleic acid sequence in a sample, characterized in that it comprises: (a) providing two nucleic acid probe sequences which are at least partially complementary to and capable of hybridizing to two adjacent regions of said target sequence; (b) hybridizing said probe sequences to said target sequence under hybridizing conditions; (c) joining said probe sequences with a ligase; d) optionally repeating the steps (b) and (c) one or more times; and (e) detecting the AMP released; wherein the presence or amount of the AMP released is indicative of the presence or amount of said target sequence.

2 (original)
A method according to claim 1, wherein said probe sequences hybridize to said target sequence to leave a gap of one or more nucleotides between adjacent probe sequences, and wherein said step (b) further comprises filling said gap by an extension reaction prior to joining said probe sequences.

3 – 4 (canceled)

5 (original)
A method according to claim 1 or 2, wherein the AMP released is detected by enzymatic means.

6 (original)
A method according to claim 1 or 2, wherein the AMP released is detected by enzymatic means comprising luciferase and luciferin.

7 (original)
A method according to claim 1 or 2, wherein the AMP released is detected by enzymatic means comprising adenylate kinase, nucleoside-diphosphate kinase, dCTP or another phosphate donor, luciferase, and luciferin.

8 (original)
A method according to claim 1 or 2, wherein said target sequence is a DNA or RNA sequence.

9 (original)
A method according to claim 1 or 2, wherein said two probe sequences are within two separate oligonucleotides.

10 (original)
A method according to claim 1 or 2, wherein said two probe sequences are the two free ends of a single oligonucleotide.

11 (original)
A method according to claim 1 or 2, wherein said target sequence is in a single-stranded form.

12 (original)
A method according to claim 1 or 2, wherein said target sequence is an amplification product.

13 (original)
A method according to claim 1 or 2, wherein at least one of said probe sequences is immobilized to a solid phase.

14 (original)
A method according to claim 1 or 2, wherein said target sequence is immobilized to a solid phase.

15 (original)
A kit for use in a method according to claim 1 or 2, characterized in that it comprises in a packaged combination: (a) a ligase, and (b) AMP detecting means.

16 - 17 (canceled)

18 (original)
A kit according to claim 15, wherein said AMP detecting means is enzymatic means.

19 (original)
A kit according to claim 15, wherein said AMP detecting means is enzymatic means comprising luciferase and luciferin.

20 (original)
A kit according to claim 15, wherein said AMP detecting means is enzymatic means comprising adenylate kinase, nucleoside-diphosphate kinase, dCTP or another phosphate donor, luciferase, and luciferin.

21 (original)
A method for detecting ligase-catalyzed joining of nucleic acid ends, characterized in that it comprises detecting by enzymatic means the AMP released.

22 (original)
A method according to claim 21, wherein said ligase is a DNA ligase.

23 (original)
A method according to claim 21, wherein said ligase is DNA ligase (NAD).

24 – 26 (canceled)

27 (original)
A method according to claim 21, wherein said enzymatic means comprises luciferase and luciferin.

28 (original)
A method according to claim 21, wherein said enzymatic means comprises adenylate kinase, nucleoside-diphosphate kinase, dCTP or another phosphate donor, luciferase, and luciferin.

29 – 44 (cancelled)